

SEQUENCE LISTING

<110> Weiner, Richard I.
 Martial, Joseph A.
 Struman, Ingrid
 Taylor, Robert
 Bentzien, Frauke

<120> Novel Antiangiogenic Peptide Agents and Their
 Therapeutic and Diagnostic Use

<130> UCSF-018/02US

<140> 09/819,094

<141> 2001-03-27

<150> 09/076,675

<151> 1998-05-12

<150> 60/046,394

<151> 1997-05-12

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tgccttcacg caccatacgt tcttcggggc ctccgatagg ataggtttcg acatctctaa 360
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act 423

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aagctatattg ccatatgggt accggccccc aagtaatggt tccggtagtt gtcgacgggtg 180
tgaagaaggg aacgggtgggg gcttctgttc ctcggttcggg ttgtctactt agtttttctg 240
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<213> Homo sapiens

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20 25 30

Leu Ser Ser Glu Met Phe Ser Glu Phe Asp Lys Arg Tyr Thr His Gly
35 40 45

Arg Gly Phe Ile Thr Lys Ala Ile Asn Ser Cys His Thr Ser Ser Leu
50 55 60

Ala Thr Pro Glu Asp Lys Glu Gln Ala Gln Gln Met Asn Gln Lys Asp
65 70 75 80

Phe Leu Ser Leu Ile Val Ser Ile Leu Arg Ser Trp Asn Glu Pro Leu
85 90 95

Tyr His Leu Val Thr Glu Val Arg Gly Met Gln Glu Ala Pro Glu Ala
100 105 110

Ile Leu Ser Lys Ala Val Glu Ile Glu Glu Gln Thr Lys Arg Leu Leu
115 120 125

Glu Gly Met Glu Leu Ile Val Ser Gln Val His Pro Glu Thr Lys Glu
130 135 140

Asn Glu Ile Tyr Pro Val Trp Ser Gly Leu Pro Ser Leu Gln Met Ala
145 150 155 160

Asp Glu Glu Ser Arg Leu Ser Ala Tyr Tyr Asn Leu Leu His Cys Leu
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Arg Ile Ile His Asn Asn Asn Cys
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<211> 124

<212> PRT

<213> Homo sapiens

<400> 10

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 20 25 30
 Leu Ser Ser Glu Met Phe Ser Glu Phe Asp Lys Arg Tyr Thr His Gly
 35 40 45
 Arg Gly Phe Ile Thr Lys Ala Ile Asn Ser Ser His Thr Ser Ser Leu
 50 55 60
 Ala Thr Pro Glu Asp Lys Glu Gln Ala Gln Gln Met Asn Gln Lys Asp
 65 70 75 80
 Phe Leu Ser Leu Ile Val Ser Ile Leu Arg Ser Trp Asn Glu Pro Leu
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 Tyr His Leu Val Thr Glu Val Arg Gly Met Gln Glu Ala Pro Glu Ala
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 Ile Leu Ser Lys Ala Val Glu Ile Glu Glu Gln Thr
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 <211> 140
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 <213> Homo sapiens

<400> 11.

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 Arg Asp Leu Phe Asp Arg Ala Val Val Leu Ser His Tyr Ile His Asn
 20 25 30
 Leu Ser Ser Glu Met Phe Ser Glu Phe Asp Lys Arg Tyr Thr His Gly
 35 40 45
 Arg Gly Phe Ile Thr Lys Ala Ile Asn Ser Ser His Thr Ser Ser Leu
 50 55 60
 Ala Thr Pro Glu Asp Lys Glu Gln Ala Gln Gln Met Asn Gln Lys Asp
 65 70 75 80
 Phe Leu Ser Leu Ile Val Ser Ile Leu Arg Ser Trp Asn Glu Pro Leu
 85 90 95
 Tyr His Leu Val Thr Glu Val Arg Gly Met Gln Glu Ala Pro Glu Ala
 100 105 110
 Ile Leu Ser Lys Ala Val Glu Ile Glu Glu Gln Thr Lys Arg Leu Leu
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Glu Gly Met Glu Leu Ile Val Ser Gln Val His Pro
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<400> 12
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Arg Asp Leu Phe Asp Arg Ala Val Val Leu Ser His Tyr Ile His Asn
 20 25 30

Leu Ser Ser Glu Met Phe Ser Glu Phe Asp Lys Arg Tyr Thr His Gly
 35 40 45

Arg Gly Phe Ile Thr Lys Ala Ile Asn Ser Ser His Thr Ser Ser Leu
 50 55 60

Ala Thr Pro Glu Asp Lys Glu Gln Ala Gln Gln Met Asn Gln Lys Asp
 65 70 75 80

Phe Leu Ser Leu Ile Val Ser Ile Leu Arg Ser Trp Asn Glu Pro Leu
 85 90 95

Tyr His Leu Val Thr Glu Val Arg Gly Met Gln Glu Ala Pro Glu Ala
 100 105 110

Ile Leu Ser Lys Ala Val Glu Ile Glu Glu Gln Thr Lys Arg Leu Leu
 115 120 125

Glu Gly Met Glu Leu Ile Val Ser Gln Val His Pro Arg Pro Pro
 130 135 140

<210> 13
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 <212> DNA
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 <213> Homo sapiens

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atgccccgacg agatgacgaa gtccttctctg tacctgttcc agctctgtaa ggacgcgtac 540
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<210> 17
<211> 192
<212> PRT
<213> Homo sapiens

<400> 17
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20 25 30
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35 40 45
Ser Gln Thr Ser Phe Cys Phe Ser Asp Ser Ile Pro Thr Pro Ser Asn
50 55 60
Met Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser
65 70 75 80
Leu Leu Leu Ile Glu Ser Trp Leu Glu Pro Val Arg Phe Leu Arg Ser
85 90 95
Met Phe Ala Asn Asn Leu Val Tyr Asp Thr Ser Asp Ser Asp Asp Tyr
100 105 110
His Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu Met Gly Arg
115 120 125
Leu Glu Asp Gly Ser Arg Arg Thr Gly Gln Ile Leu Lys Gln Thr Tyr
130 135 140
Ser Lys Phe Asp Thr Asn Ser His Asn His Asp Ala Leu Leu Lys Asn
145 150 155 160
Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr
165 170 175
Phe Leu Arg Met Val Gln Cys Arg Ser Val Glu Gly Ser Cys Gly Phe
180 185 190

<210> 18
<211> 135
<212> PRT

<213> Homo sapiens

<400> 18

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1 5 10 15

Gln Ala His Arg Ala His Gln Leu Ala Ile Asp Thr Tyr Gln Glu Phe
20 25 30

Glu Glu Thr Tyr Ile Pro Lys Asp Gln Lys Tyr Ser Phe Leu His Asp
35 40 45

Ser Gln Thr Ser Phe Ser Phe Ser Asp Ser Ile Pro Thr Pro Ser Asn
50 55 60

Met Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser
65 70 75 80

Leu Leu Leu Ile Glu Ser Trp Leu Glu Pro Val Arg Phe Leu Arg Ser
85 90 95

Met Phe Ala Asn Asn Leu Val Tyr Asp Thr Ser Asp Ser Asp Asp Tyr
100 105 110

His Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu Met Gly Arg
115 120 125

Leu Glu Asp Gly Ser Pro Arg
130 135

<210> 19

<211> 579

<212> DNA

<213> Homo sapiens

<400> 19

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<212> DNA

<213> Homo sapiens

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<212> DNA
<213> Homo sapiens

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tgtgggaggt tgtccctcct ttgtgttgtc tttaggttgg atctcgacga ggcgtagagg 240
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tcggaccaca tgccgcggag actgtcgttg cagatactgg aggatttcct ggatctcctt 360
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<212> DNA
<213> Homo sapiens

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gtcttcataa gtaaggacgt cttgggggtc tggagggaga caaagagtct cagataaggc 180
tgtgggaggt tgtccctcct ttgtgttgtc tttaggttgg atctcgacga ggcgtagagg 240
gacgacgagt aggtcagcac cgacctcggg cacgtcaagg agtcctcaca gaagcggttg 300
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<212> PRT
<213> Homo sapiens

<400> 23
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20 25 30

Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn
 35 40 45
 Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn
 50 55 60
 Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser
 65 70 75 80
 Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe Leu Arg Ser
 85 90 95
 Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn Val Tyr
 100 105 110
 Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu Met Gly Arg
 115 120 125
 Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys Gln Thr Tyr
 130 135 140
 Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu Leu Lys Asn
 145 150 155 160
 Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr
 165 170 175
 Phe Leu Arg Ile Val Gln Cys Arg Ser Val Glu Gly Ser Cys Gly Phe
 180 185 190

<210> 24
 <211> 134
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<400> 24
 Met Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe Asp Asn Ala Met Leu
 1 5 10 15
 Arg Ala His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr Gln Glu Phe
 20 25 30
 Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn
 35 40 45
 Pro Gln Thr Ser Leu Ser Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn
 50 55 60

Arg Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser
65 70 75 80

Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe Leu Arg Ser
85 90 95

Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn Val Tyr
100 105 110

Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu Met Gly Arg
115 120 125

Leu Glu Asp Gly Ser Pro
130

<210> 25
<211> 579
<212> DNA
<213> Homo sapiens

<400> 25
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ctgtaccagc tggcatatga cacctatcag gagtttgaag aagcctatat cctgaaggag 120
cagaagtatt cattcctgca gaacccccag acctccctct gcttctcaga gtctattcca 180
acaccttcca acagggtgaa aacgcagcag aaatctaacc tagagctgct ccgcatctcc 240
ctgctgctca tccagtcag gctggagccc gtgcagctcc tcaggagcgt cttcgccaac 300
agcctgggtg atggcgctc ggacagcaac gtctatcgcc acctgaagga cctagaggaa 360
ggcatccaaa cgctgatgtg gaggctggaa gatggcagcc ccgggactgg gcagatcttc 420
aatcagtcct acagcaagtt tgacacaaaa tgcacaacg atgacgcact gctcaagaac 480
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gtgcagtgcc gctctgtgga gggcagctgt ggcttctag 579

<210> 26
<211> 579
<212> DNA
<213> Homo sapiens

<400> 26
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ctgtaccagc tggcatatga cacctatcag gagtttgaag aagcctatat cctgaaggag 120
cagaagtatt cattcctgca gaacccccag acctccctct gcttctcaga gtctattcca 180
acaccttcca acagggtgaa aacgcagcag aaatctaacc tagagctgct ccgcatctcc 240
ctgctgctca tccagtcag gctggagccc gtgcagctcc tcaggagcgt cttcgccaac 300
agcctgggtg atggcgctc ggacagcaac gtctatcgcc acctgaagga cctagaggaa 360
ggcatccaaa cgctgatgtg gaggctggaa gatggcagcc ccgggactgg gcagatcttc 420
aatcagtcct acagcaagtt tgacacaaaa tgcacaacg atgacgcact gctcaagaac 480
tacgggctgc tctactgctt caggaaggac atggacaagg tcgagacatt cctgcgcatac 540
gtgcagtgcc gctctgtgga gggcagctgt ggcttctag 579

<210> 27

<211> 579
 <212> DNA
 <213> Homo sapiens

<400> 27
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 gacatgggtcg accgtatact gtggatagtc ctcaaacttc ttcggatata ggacttcctc 120
 gtcttcataa gtaaggacgt cttgggggtc tggagggaga cgaagagtct cagataaggt 180
 tgtggaaggt tgtcccaactt ttgctcgtc tttagattgg atctcgacga ggcgtagagg 240
 gacgacgagt aggtcagtag cgacctcggg cagctcgagg agtcctcgca gaagcgggtg 300
 tcggaccaca taccgcggag cctgtcgttg cagatagcgg tggacttcct ggatctcctt 360
 ccgtagggttt gcgactacac ctccgacctt ctaccgtcgg gggcctgacc cgtctagaag 420
 ttagtcagga tgtcgttcaa actgtgtttt agcgtgttgc tactgcgtga cgagttcttg 480
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 cacgtcacgg cgagacacct cccgtcgaca ccgaagatc 579

<210> 28
 <211> 579
 <212> DNA
 <213> Homo sapiens

<400> 28
 tacaaggggtt ggtaagggaa taggtccgaa aaactggtgc gatacgaggc gcgggcagcg 60
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 gtcttcataa gtaaggacgt cttgggggtc tggagggaga cgaagagtct cagataaggt 180
 tgtggaaggt tgtcccaactt ttgctcgtc tttagattgg atctcgacga ggcgtagagg 240
 gacgacgagt aggtcagtag cgacctcggg cagctcgagg agtcctcgca gaagcgggtg 300
 tcggaccaca taccgcggag cctgtcgttg cagatagcgg tggacttcct ggatctcctt 360
 ccgtagggttt gcgactacac ctccgacctt ctaccgtcgg gggcctgacc cgtctagaag 420
 ttagtcagga tgtcgttcaa actgtgtttt agcgtgttgc tactgcgtga cgagttcttg 480
 atgcccgaag agatgacgaa gtccttcctg tacctgttcc agctctgtaa ggacgcgtag 540
 cacgtcacgg cgagacacct cccgtcgaca ccgaagatc 579

<210> 29
 <211> 192
 <212> PRT
 <213> Homo sapiens

<400> 29
 Met Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe Asp Asn Ala Met Leu
 1 5 10 15
 Arg Ala Arg Arg Leu Tyr Gln Leu Ala Tyr Asp Thr Tyr Gln Glu Phe
 20 25 30
 Glu Glu Ala Tyr Ile Leu Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn
 35 40 45
 Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn
 50 55 60
 Arg Val Lys Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser

65		70		75		80									
Leu	Leu	Leu	Ile	Gln	Ser	Trp	Leu	Glu	Pro	Val	Gln	Leu	Leu	Arg	Ser
				85					90					95	
Val	Phe	Ala	Asn	Ser	Leu	Val	Tyr	Gly	Ala	Ser	Asp	Ser	Asn	Val	Tyr
			100					105					110		
Arg	His	Leu	Lys	Asp	Leu	Glu	Glu	Gly	Ile	Gln	Thr	Leu	Met	Trp	Arg
		115					120					125			
Leu	Glu	Asp	Gly	Ser	Pro	Arg	Thr	Gly	Gln	Ile	Phe	Asn	Gln	Ser	Tyr
	130					135					140				
Ser	Lys	Phe	Asp	Thr	Lys	Ser	His	Asn	Asp	Asp	Ala	Leu	Leu	Lys	Asn
145					150					155					160
Tyr	Gly	Leu	Leu	Tyr	Cys	Phe	Arg	Lys	Asp	Met	Asp	Lys	Val	Glu	Thr
				165					170					175	
Phe	Leu	Arg	Ile	Val	Gln	Cys	Arg	Ser	Val	Glu	Gly	Ser	Cys	Gly	Phe
			180					185					190		

<210> 30
 <211> 135
 <212> PRT
 <213> Homo sapiens

<400> 30
Met Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe Asp Asn Ala Met Leu
1 5 10 15
Arg Ala Arg Arg Leu Tyr Gln Leu Ala Tyr Asp Thr Tyr Gln Glu Phe
20 25 30
Glu Glu Ala Tyr Ile Leu Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn
35 40 45
Pro Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn
50 55 60
Arg Val Lys Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser
65 70 75 80
Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Leu Leu Arg Ser
85 90 95
Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn Val Tyr

100	105	110
Arg His Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu Met Trp Arg		
115	120	125

Leu Glu Asp Gly Ser Pro Arg
130 135

<210> 31
 <211> 18
 <212> DNA
 <213> Homo sapiens

<400> 31
 cctgaaacca aagaaaat 18

<210> 32
 <211> 6
 <212> PRT
 <213> Homo sapiens

<400> 32
 Pro Glu Thr Lys Glu Asn
 1 5

<210> 33
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: nucleotide
 sequence coding for specific cleavage site of the
 IgA protease

<400> 33
 cctagacccc caacacct 18

<210> 34
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: specific
 cleavage site of the IgA protease

<400> 34
 Pro Arg Pro Pro Thr Pro
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